We have identified Mbnl2 mediated splicing events and mRNA expression regulation by comparing WT and Mbnl2 ΔE2/ΔE2 mouse hippocampii using Affymetrix Mouse Exon Junction Array and mRNA sequencing. These data are included in the same study titled "Muscleblind-Like 2 Mediated Alternative Splicing in the Developing Brain and Dysregulation in Myotonic Dystrophy" now in cell press to be published in Neuron. The splicing microarray data has already been submitted under GSE37908 which also includes a re-analysis of RNA-seq data.

Table S1. Splicing microarray analysis of *Mbnl2*$^{+/+}$ versus *Mbnl2*$^{\Delta E2/\Delta E2}$ knockout hippocampus.

(A) Splicing microarray summary of alternative cassette exons mis-spliced in *Mbnl2* knockouts.
(B) RNA-seq and splicing microarray analysis ($p<0.05$).
(C) Genes (n=68) identified by splicing microarrays ($p<0.05$).
(D) Genes (n=39) with $p<0.05$ and sepscore>0.3.

Table S2. RNA-Seq, Gene Ontology, HITS-CLIP and CIMS summary of *Mbnl2*$^{+/+}$ versus *Mbnl2*$^{\Delta E2/\Delta E2}$ knockout hippocampus.

(A) RNA-seq summary.
(B) RNA-seq targets with 179 high-confidence Mbnl2-dependent cassette exons identified from RNA-seq (junction coverage≥20, FDR≤0.05, $|\Delta I|\geq 0.1$).
(C) Joint target alternative splicing including 267 combined high-confidence Mbnl2-dependent cassette exons annotated in our alternative splicing database (AS db).
(D) Mjay targets not included in AS db.
(E) Joint target genes including 249 genes with high-confidence Mbnl2-dependent splicing identified by splicing microarray or RNA-seq.
(F) Gene Ontology analysis using 249 Mbnl2 target transcripts compared to all genes expressed in hippocampus. Terms with Benjamini FDR≤0.05 are listed.